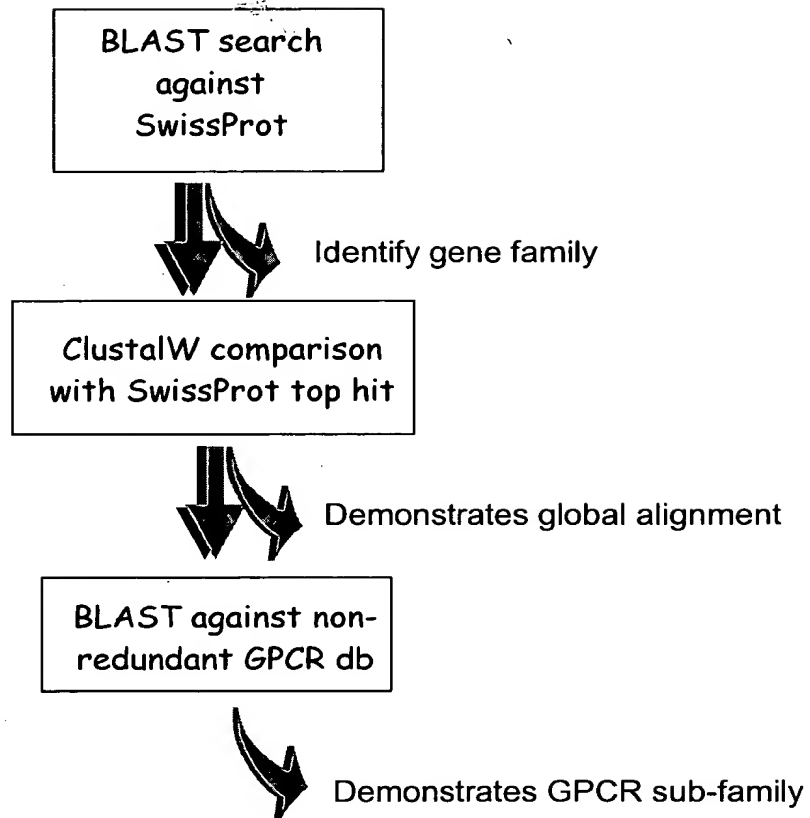


APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 1



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 3

CLUSTAL W (1.74) multiple sequence alignment

```

NTR1_RAT      MHLNSSVPQGTGPEPDAQPFSGPQSEMEATFLALSLSNGSGNTSESDTAGPNSDLDVNTD
PFI-002      -----MEKLQNASWIYQQKLEDPFQKH-----LNSTEEYLAFLCGPRRS---
               *   .   *   .   *   .   *   .   *   .   *   .

NTR1_RAT      IYSKVLVTAIYLALFVVGTGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDDLILLLA
PFI-002      HF-FLPVSVVYVPIFVVGVIGNVLVCLVILQ---HQAMKTPTNYLFSLAVSDLLVLLLG
               :   :   *   .   .   .   .   .   .   .   .   .   .   .   .   .   .
               :   :   *   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      MPVELYNFIWVHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHFPKAKTL
PFI-002      MPLEVY-EMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVRYVAILHFPRAKLQ
               *   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
               *   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      MSRSRTKKFISAIWLASALLAIPMLFTMGLQN-RSGDG-THPGGLVCTPIVDTATVKVVI
PFI-002      STRRRALRILGIVWGFSVLFSLPNTSIHGKIFHYFPNGSLVPGSATCTVIKPMWIYNFII
               :   *   :   .   .   .   .   .   .   .   .   .   .   .   .   .
               :   *   :   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      QVNTFMSFLFPMLVISILNTVIANKLTVMVHQAAEQGRVCTVGTHNGLEHSTFNMTIEPG
PFI-002      QVTSFLFYLLPMTVISVLYYLMALR-----
               *   .   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      RVQALRHGVLVLRAVVIAFVVCWLPYHVRRLMFCYISDEQWTTFLDFYHYFYMLTNALF
PFI-002      -----
               :   :   :   :   :   :   :   :   :   :   :   :   :   :   :

NTR1_RAT      YVSSAINPILYNLVSANFRQVFLSTLACLCPGWRHRRKKRPTFSRKPNMSSNHAFSTSA
PFI-002      -----
               :   :   :   :   :   :   :   :   :   :   :   :   :   :   :

NTR1_RAT      TRETLY
PFI-002      -----

```


APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 5

Figure 5A

Nucleotide sequence coding for PFI-002

SEQ ID NO: 1

ATGGAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAACTAGAAGATC
CATTCCAGAAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGG
ACCTCGGCGCAGCCACTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTT
TGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACC
AGGCTATGAAGACGCCACCACTACTACCTCTTCAGCCTGGCGGTCTCTGA
CCTCCTGGTCCTGCTCCTTGGAATGCCCTGGAGGTCTATGAGATGTGGCGCA
ACTACCCTTTCTTGTTTCGGGCCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTT
GAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGC
GCTACGTGGCCATCCTACACCCGTTCCGCGCCAACTGCAGAGCACCCGGCG
CCGGGCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCC
TGCCCAACACCAGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCC
CTGGTCCCAGGTTTCGGCCACCTGTACGGTCATCAAGCCCATGTGGATCTACA
ATTTTCATCATCCAGGTCACCTCCTTCTATTCTACCTCCTCCCCATGACTGTCA
TCAGTGTCTCTACTACCTCATGGCACTCAGAGTGAGTATCTAG

Figure 5B

Amino acid sequence coding for PFI-002

SEQ ID NO: 2

MEKLQNASWIYQQKLEDPFQKHLNSTEYLAFLCGPRRSHFFLPVSVVYVPIFVV
GVIGNVLVCLVILQHQAAMKTPNTNYLFS LAVSDLLVLLGMPLEVYEMWRNYPF
LFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGI
VWGFSVLFSLPNTSIHGKIFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYI
LPMTVISVLYYLMALRVSI

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 6

SEQ ID NO: 3
ACCATGGCAGGGATGGAAAACTT

SEQ ID NO: 4
GCTCTGAAAGAATTCAGGTTTTG

SEQ ID NO: 5
TCCAGAAACACCTGAACAGC

SEQ ID NO: 6
GAGGTAGAATAGGAAGGAGG

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